EXHIBIT F

IN THE UNITED STATES DISTRICT COURT

IN AND FOR THE DISTRICT OF DELAWARE

TWINSTRAND BIOSCIENCES, INC. & UNIVERSITY OF WASHINGTON,	)	
Plaintiffs,	)	C.A. No. 21-1126-GBW
V.	)	
GUARDANT HEALTH, INC.,	)	
Defendant.	)	

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Wilmington, Delaware
Monday, November 6, 2023
Trial Transcript Volume 1

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BEFORE: HONORABLE GREGORY B. WILLIAMS
UNITED STATES DISTRICT COURT JUDGE

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APPEARANCES:

YOUNG CONAWAY STARGATT & TAYLOR, LLP
By: ADAM W. POFF, ESQ.
SAMANTHA G. WILSON, ESQ.

-and-

STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
By: BYRON L. PICKARD, ESQ.
R. WILSON POWERS III, PH.D., ESQ.
CHANDRIKA VIRA, ESQ.
WILLIAM H. MILLIKEN, ESQ.
ANNA G. PHILLIPS, ESQ.
TYLER J. DUTTON, ESQ.

For the Plaintiff

DLA PIPER LLP
BY: BRIAN A. BIGGS, ESQ.
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MARK FOWLER, ESQ.
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ELLEN SCORDINO, ESQ.

For the Defendant

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P R O C E E D I N G S

(REPORTER'S NOTE: The following hearing was held in Courtroom 6B, beginning at 9:00 a.m.)

THE COURT: Good morning.

ALL COUNSEL: Good morning, Your Honor.

THE COURT: You may be seated.

The Court received the parties' joint submissions that parties didn't have any objections this morning, but wanted some guidance on a few issues, so let's go through those issues.

First, with respect to the Court's construction of "each," on Guardant's motion for summary judgment, the parties should present that according to -- present all these terms according to the Court's claim construction, but with respect to that particular term "each," the Court construed it according to its plain and ordinary meaning, but with the finding that it does not require 100 percent efficiency.

Moreover, Guardant cannot argue during trial that each requires that all molecules are ligated because that would be inconsistent with the Court's claim construction.

Second, with respect to the Court's construction on ordering of steps. With respect to the '127 patent, that

way of a subsequent comparison where are there any differences.

And, again, this is just a diagram. The human genome, as I said, is enormous, so you don't -- you don't line it up like those, you know -- like those find-the-difference in the Sunday newspaper. I like those. So you don't do it that way, but you use a computer to do essentially the same task.

Q. Okay. And what's on this demonstrative, Dr. Pachter?

A. So here I'm showing you what some actual data might look like. On the horizontal line here, on the axis, you see labeled different genome positions, so these are many, many positions indicated here, more than 3,500. Of course, this -- again, this is still a tiny part of the whole human genome.

And on the vertical lines here is essentially, in some unit, some measure of how much difference you're seeing.

Q. Does this represent noise?

A. Yeah, so a lot of -- not all of it, but most of this difference is not mutation, but it's just noise from the machine randomly changing some of those (As), (Cs), (Gs), and (Ts) to where you see a difference, but it's not really a mutation, it's just noise.

Q. And what are we seeing here?

A. **So you've just seen the noise suppressed and dropped down. That's what the invention of the University of Washington teaches you to do. It's a way to get rid just of the noise without throwing away the signal, which is the actual mutation you're looking at. After you do that process, you can go, Oh, ah-ha, right here, at position 1000, that was an actual difference in the patient and not just an error that came out of my not-so-good sequencing machine.**

Q. **What's on this demonstrative, Dr. Pachter?**

A. **So here I made a diagram just to show you at a high level how this invention works.**

Q. **Okay. And can you start off and kind of walk us through what you're showing?**

A. **Yeah, so on the left-hand side here -- we'll start over here -- there is a representation of a DNA molecule, so this would have been a molecule that was extracted from a biosample. In the invention, there will be a population, many such molecules. And you can see that there's a top and a bottom. These are the two strands of those ribbons. And in the invention, there's this gadget on the left here and that's a synthetic, custom-made, that's a key part of the invention that gets attached to that DNA molecule.**

Q. **What does attaching this custom-made piece of DNA get you?**

A. **So there's really two goals. One of the things you'd like to do is you'd like to barcode this molecule. That means you -- a barcode here is a little bit of sequence, and that's in the blue and the red here, or orange. And you're attaching that on so that after you do the sequencing, you'll be able to go back and find those barcodes for a lot of different molecules and be able to tell, oh, all those sequences were from the same molecule.**

Q. **What happens next in the workflow?**

A. **Right. So what happens next in the workflow -- that's key to what I just said -- is that there's what's called amplification. That's copying -- these molecules get copied, and that's just necessary for the sequencer to work. It's a technical thing. So that's why you're going to have lots of copies of the same molecule, but they're not coming out in the same order. You got to go back and figure out which sequences were actually from the same molecule, and the barcodes, these barcodes, the blue and orange, they let you do that.**

Q. **I notice you call them top and bottom strands here. Is that the same as Watson and Crick strands?**

A. **Yes, that's exactly the same thing. The DNA double-helix was discovered by several people, but two of them were -- were named Dr. Watson and Dr. Crick, and it's noted after them. And I apologize a bit on behalf of my**

field. We give lots of different names to the same thing and it can be confusing, but it's just -- just the same thing.

Q. You mentioned the Y-shaped adapters allow you to distinguish between the top strand and bottom strands. Can you explain that a little bit?

A. Yeah, so I've talked so far, if you recall, about the barcodes to go back and figure out which sequences were from the same molecule. But there's this Y-shaped end at -- bit at the end, and this Y-shaped bit, it's got another purpose. If you recall, there were two different goals with this gadget, and its purpose is to be able to distinguish which sequences came from the top strand here, or the Watson, and which ones came from the bottom.

Q. How do those purple and green parts let you do that?

A. So first of all, again, the purple and green colors here just signify a sequence, a different sequence. You can see here that orange and orange, that's the same sequence paired up together, but here purple and green are different, and that's why it looks like a Y like this, because the sequences are different. In the jargon, we call it noncomplementary. If they were the same, they would be lined up, but they're different, so that's the Y-shaped.

Q. And what's happening in the middle part of this schematic?

A. **So this is showing you how, after you've done the sequencing, you can use the purple and the green to tell apart the strands.**

Q. **How do you do that?**

A. **So if you look at all of the -- all of the molecules on the top strand, if you read them from left to right, the colors are purple, blue, and then orange, green. But on the bottom strand, the colors are green, blue, and then orange, purple. And so the green here is paired with the blue. Here it's paired with the orange, and they're in different order.**

So after you sequence, by looking at these sequences that you put in and knowing what they are and these barcodes, you can -- you can separate out the sequences over the top strand and the bottom strand.

Q. **And what are those red dots?**

A. **So the red dots are a showing how you might get error coming out of the sequencer. So now, you know, you didn't get the exact molecule, maybe in this red dot over here. It's not a mutation in the patient or anything; it's just an (A) got switched maybe to a (C), and those are the red dots.**

Q. **And then what happens next in the schematic?**

A. **So what happens next, you'll see it says, "compare the top and the bottom strands," so by comparing these individual sequences -- they're also called reads -- you can**

clean out these red dots and eliminate the errors. One way I like to think about it is that these red dots, they're sort of like lightning strikes. But if you have, you know, a real mutation, you're going to have the same changes on the top and the bottom strand, and that's very, very unlikely that lightning strikes over and over exactly at the same place. And so at the end, you get, by this process, a high-accuracy consensus and you've eliminated the errors.

Q. Thank you, Dr. Pachter.

What are we seeing here?

A. So here on the left-hand side, I'm showing you -- this is PTX835, page 2. You've seen this diagram before. This is from the University of Washington invention showing how all this noise was suppressed by the invention, by the duplex sequencing method to leave the real mutation.

And on the right-hand side, this is an image from a Guardant Health document, JTX022, that's showing the same -- the same thing.

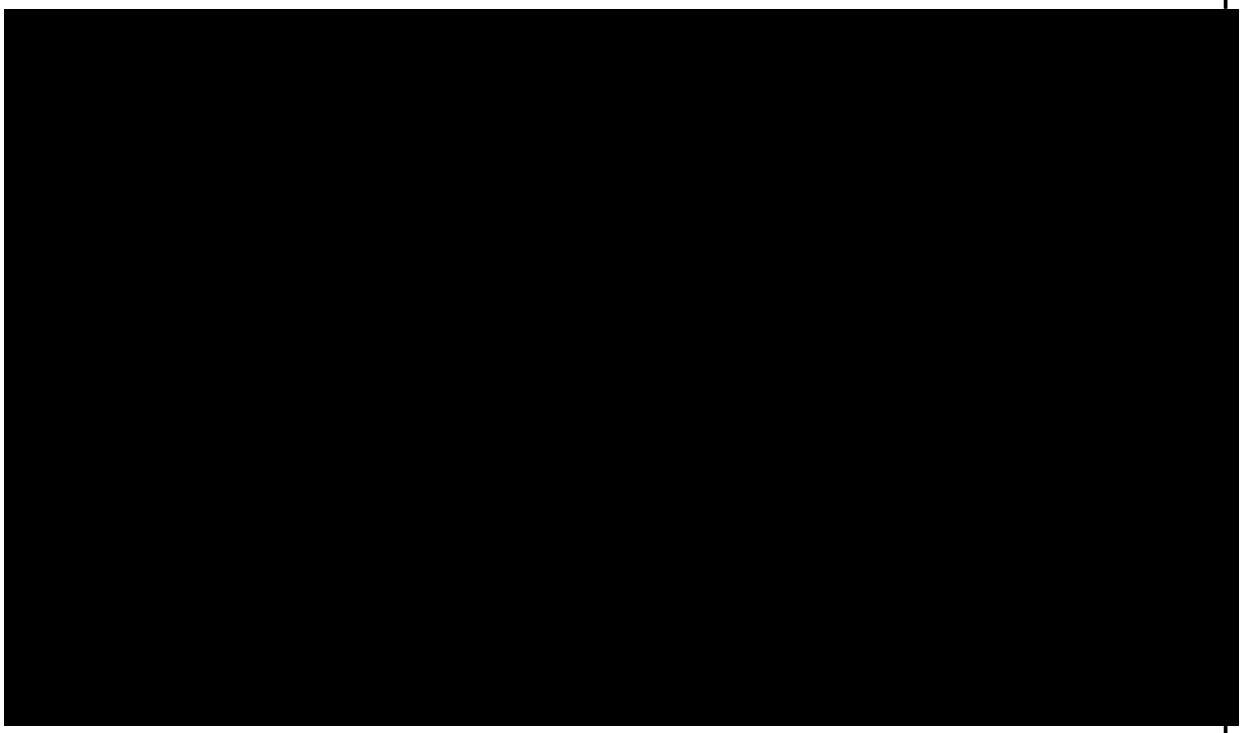
Q. So in the bottom part of both of these slides, both of these demonstratives -- sorry, both sides of this demonstrative is showing errors eliminated?

A. Yeah, so what you're seeing here is that Guardant also is using next-generation sequencing. It also has errors. Here there -- there are these dots here that we see. Again, their suppression has squished them all down to

A. **Yes, absolutely.**

Q. **Okay. What are we seeing here, Dr. Pachter?**

Q. **And what is this demonstrative showing, Dr. Pachter?**



Q. **So can we put a check by this one?**

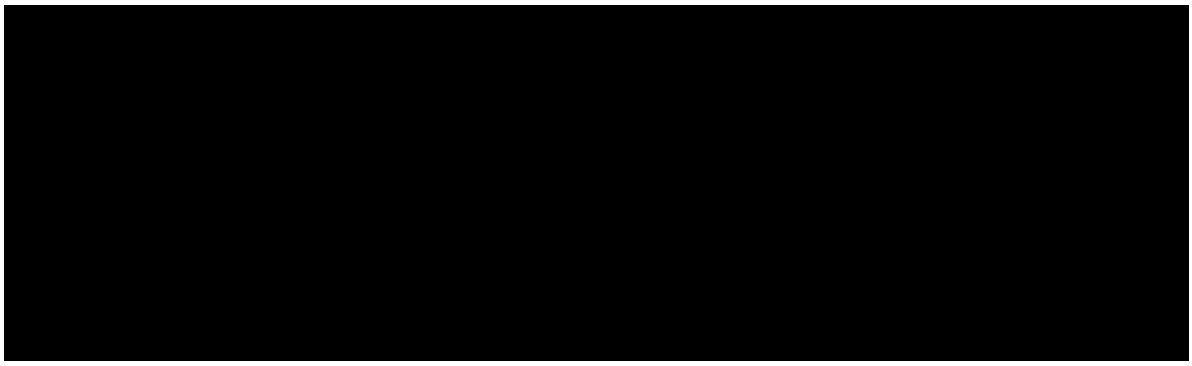
A. **Yes, we can.**

Q. **What's the next step in the claim?**

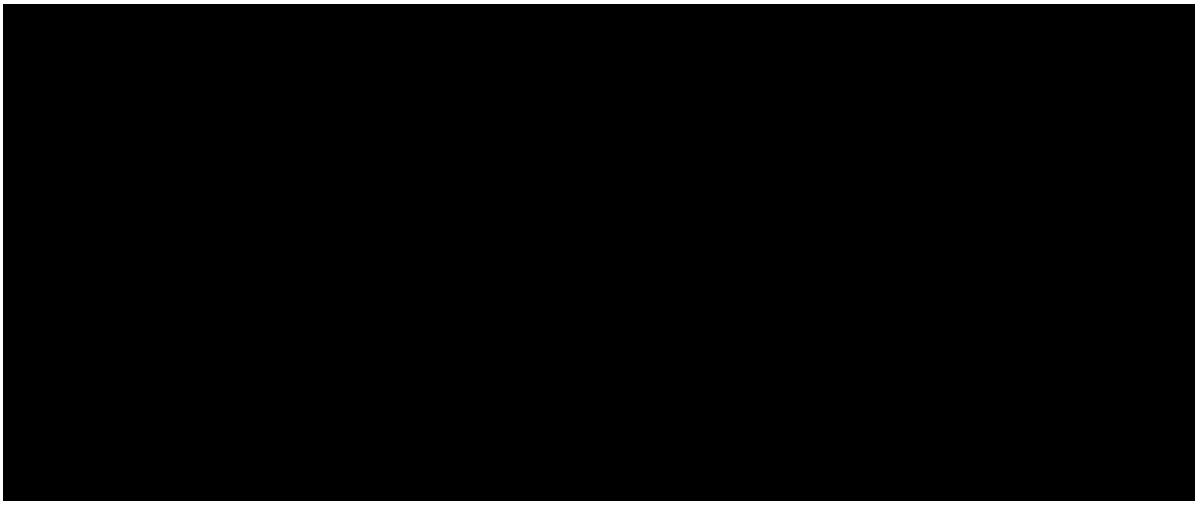
A. **Again, in order to do the sequencing first, we have to amplify or copy the molecules, that's the next**

amplification step.

Q. All right. And what are we seeing on this demonstrative?



Q. And what are we seeing in this demonstrative, Dr. Pachter?



Q. So can we put a check by this one?

A. Yes, we can.

Q. Okay. What's the next step in the claim?

A. So we're almost done with the stuff from the test tube. Now it's going in the sequencer. This step calls for sequencing.

Q. Did you find evidence that Guardant's products and services use sequencing?

[redacted]

Q. **So can we put a check by this one?**

A. **Yes, we can.**

Q. **What's this next element, Dr. Pachter?**

A. **So now we're done with the test tube, we're done with the sequencing. But we've got the information now on our molecules, those tags that had the barcodes or the SMIs, in the strand-distinguishing sequences. So now we're going to start again with the bioinformatics. And this claim, it begins by asking for the grouping.**

Q. **Did you find evidence for grouping in Guardant's products and services?**

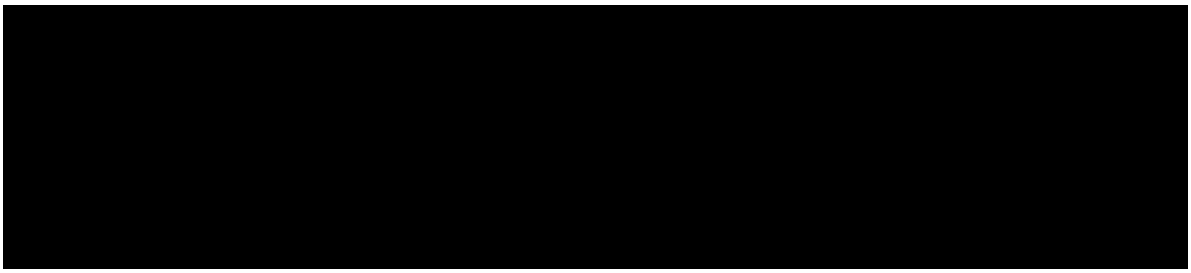
[redacted]

Q. **What's on this demonstrative, Dr. Pachter?**

[redacted]

Q. **And what are we seeing here, Dr. Pachter?**

Q. **What's on this demonstrative?**



Q. **So can we put a checkmark by this claim element?**

A. **Yes, we can.**

Q. **Okay. What 's this next claim element, Dr. Pachter?**

A. **So next, in order to be able to use the strand information, the claim is asking for separating the first and second strand sequences. I call this the separating**

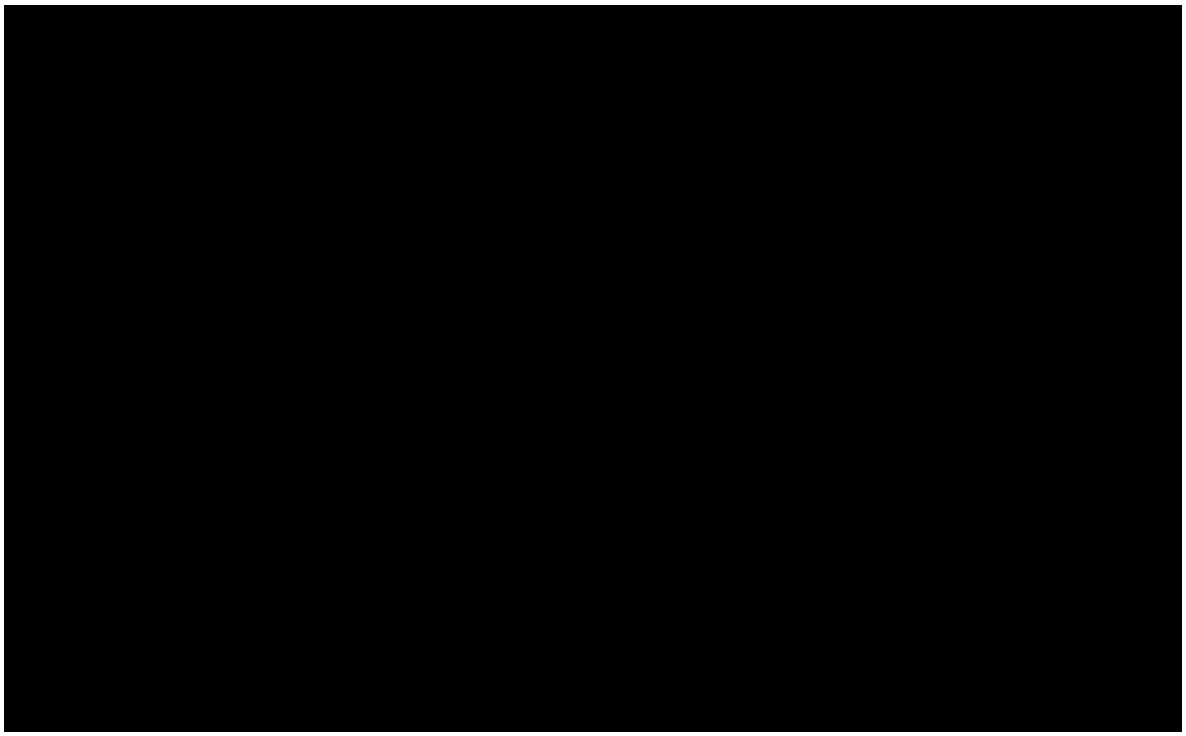
step.

Q. **And did you find evidence for the separating step in Guardant's products and services?**

A. **Yes, I did.**

Q. **What's on this demonstrative, what do we see?**

Q. **What are we seeing on this demonstrative, Dr. Pachter?**



[redacted]

Q. **What are we seeing on this demonstrative, Dr. Pachter?**

[redacted]

Q. **Well, Dr. Pachter, are these strands being physically separated?**

[redacted]